```
================================================================
Sequence Listing could not be accepted.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: [year=2010; month=7; day=27; hr=9; min=43; sec=57; ms=320; ]
================================================================



*************************************************************
Reviewer Comments:
<210>   57
<211>   10
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Synthetic


<220>
<221>   misc_feature
<222>   (1)..(1)
<223>   n is glycine or alanine.

<220>
<221>   misc_feature
<222>   (7)..(7)
<223>   n is threonine or cysteine.

<220>
<221>   misc_feature
<222>   (8)..(8)
<223>   n is threonine or cysteine.

<400>   57
nggaganntg
10


The above <220>-<223> sections describing the "n's" are errored:   "n"
can only represent a single nucleotide; it cannot represent an amino
```

acid.

<210> 130
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> X can be a or g.

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> X can be t or c.

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> X can be a or g.

<400> 130

Xaa Gly Gly Ala Gly Ala Xaa Thr Thr Xaa
1   5   10

If the above <220>-<223> sections regarding the "Xaa's" are defining
them as nucleotides, they are erroneous. If they are denoting amino
acids, please spell them out in the <223> responses.
****

Application No: 10574333   Version No: 1.0

                        Input Set:

                        Output Set:

                    Started: 2010-07-21 14:54:12.726
                    Finished: 2010-07-21 14:54:16.948
                    Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 222 ms
            Total Warnings: 100
              Total Errors: 0
    No. of SeqIDs Defined: 134
        Actual SeqID Count: 134

Error code   Error Description

W   213   Artificial or Unknown found in <213> in SEQ ID (21)

W   213   Artificial or Unknown found in <213> in SEQ ID (22)

W   213   Artificial or Unknown found in <213> in SEQ ID (23)

W   213   Artificial or Unknown found in <213> in SEQ ID (24)

W   213   Artificial or Unknown found in <213> in SEQ ID (25)

W   213   Artificial or Unknown found in <213> in SEQ ID (26)

W   213   Artificial or Unknown found in <213> in SEQ ID (27)

W   213   Artificial or Unknown found in <213> in SEQ ID (28)

W   213   Artificial or Unknown found in <213> in SEQ ID (29)

W   213   Artificial or Unknown found in <213> in SEQ ID (30)

W   213   Artificial or Unknown found in <213> in SEQ ID (31)

W   213   Artificial or Unknown found in <213> in SEQ ID (32)

W   213   Artificial or Unknown found in <213> in SEQ ID (33)

W   213   Artificial or Unknown found in <213> in SEQ ID (34)

W   213   Artificial or Unknown found in <213> in SEQ ID (35)

W   213   Artificial or Unknown found in <213> in SEQ ID (36)

W   213   Artificial or Unknown found in <213> in SEQ ID (37)

W   213   Artificial or Unknown found in <213> in SEQ ID (38)

W   213   Artificial or Unknown found in <213> in SEQ ID (39)

W   213   Artificial or Unknown found in <213> in SEQ ID (40)

```
        Input Set:


        Output Set:



           Started:  2010-07-21 14:54:12.726
          Finished:  2010-07-21 14:54:16.948
           Elapsed:  0 hr(s) 0 min(s) 4 sec(s) 222 ms
    Total Warnings:  100
      Total Errors:  0
No. of SeqIDs Defined:  134
 Actual SeqID Count:  134
```

Error code   Error Description

```
        This error has occured more than 20 times, will not be displayed
```

SEQUENCE LISTING

<110>   The Regents of the University of California
        Karin, Michael
        Bonizzi, Giussepina
        Bebien, Mahali

<120>   Compositions and Methods for Gene Expression

<130>   UCSD-10835

<140>   10574333
<141>   2010-07-21

<150>   US 60/508349
<151>   2003-10-01

<150>   PCT/US2004/032246
<151>   2004-09-29

<160>   134

<170>   PatentIn version 3.5

<210>   1
<211>   700
<212>   DNA
<213>   Mus musculus

<400>   1
ttcgtaccat ccacccaccc ccagtcgaga gaataggggt acagagggga ggtggcaaag   60

aaaattcacg atactgagta tctctgggag acctgtttgg tctctttgct cggtagcgca   120

gccctacgtt agaatgcatc ttcccgggaa tgactgtagt gagactttgg ctgggaatcc   180

aagttattct aactgtagat tggtccacgt tgccctaagc ctagcagtcc actgcggcac   240

agacaccctg gacatgaggt gggtcagctt aagttcctgg cacgaaagaa agggtactct   300

ggcaactttt ggatgcggcg aaacagactg tttcgtctct caggttctta tttcacggct   360

tgtgcctttg acagcccctt agtttctcta tctgcaggat gggagcatta agctctacga   420

cccagcctct ttacaattca ggtccaaaga gcccgcccaa gttggggact gggaagatca   480

aaggtctcag cacccagcgg agccgcggac actgagggcg ccaagaaggg ggtgggtagg   540

tagggaactg gaagggcggc tgctccgcag gggatgcgcg tcagagaccc cagccacact   600

ccaggcccgc cccttgatga gccccgcccc gccccgcctg gttttcgcct ctaaagcgcc   660

cagcgctcgc ctcccgctgc cgcactttca ctctcggtcc   700

<210>   2

<210> 10

<211> 10

<212> DNA

<213> Mus musculus

<400> 2

gggagacctg   10

<210> 3

<211> 933

<212> PRT

<213> Homo sapiens

<400> 3

Met Glu Ser Cys Tyr Asn Pro Gly Leu Asp Gly Ile Ile Glu Tyr Asp
1   5   10   15

Asp Phe Lys Leu Asn Ser Ser Ile Val Glu Pro Lys Glu Pro Ala Pro
            20   25   30

Glu Thr Ala Asp Gly Pro Tyr Leu Val Ile Val Glu Gln Pro Lys Gln
        35   40   45

Arg Gly Phe Arg Phe Arg Tyr Gly Cys Glu Gly Pro Ser His Gly Gly
    50   55   60

Leu Pro Gly Ala Ser Ser Glu Lys Gly Arg Lys Thr Tyr Pro Thr Val
65   70   75   80

Lys Ile Cys Asn Tyr Glu Gly Pro Ala Lys Ile Glu Val Asp Leu Val
                85   90   95

Thr His Ser Asp Pro Pro Arg Ala His Ala His Ser Leu Val Gly Lys
            100   105   110

Gln Cys Ser Glu Leu Gly Ile Cys Ala Val Ser Val Gly Pro Lys Asp
        115   120   125

Met Thr Ala Gln Phe Asn Asn Leu Gly Val Leu His Val Thr Lys Lys
    130   135   140

Asn Met Met Gly Thr Met Ile Gln Lys Leu Gln Arg Gln Arg Leu Arg
145   150   155   160

Ser Arg Pro Gln Gly Leu Thr Glu Ala Glu Gln Arg Glu Leu Glu Gln
                165   170   175

Glu Ala Lys Glu Leu Lys Lys Val Met Asp Leu Ser Ile Val Arg Leu
            180   185   190

Arg Phe Ser Ala Phe Leu Arg Ala Ser Asp Gly Ser Phe Ser Leu Pro
            195   200   205

Leu Lys Pro Val Thr Ser Gln Pro Ile His Asp Ser Lys Ser Pro Gly
    210   215   220

Ala Ser Asn Leu Lys Ile Ser Arg Met Asp Lys Thr Ala Gly Ser Val
225   230   235   240

Arg Gly Gly Asp Glu Val Tyr Leu Leu Cys Asp Lys Val Gln Lys Asp
            245   250   255

Asp Ile Glu Val Arg Phe Tyr Glu Asp Asp Glu Asn Gly Trp Gln Ala
            260   265   270

Phe Gly Asp Phe Ser Pro Thr Asp Val His Lys Gln Tyr Ala Ile Val
            275   280   285

Phe Arg Thr Pro Pro Tyr His Lys Met Lys Ile Glu Arg Pro Val Thr
    290   295   300

Val Phe Leu Gln Leu Lys Arg Lys Arg Gly Gly Asp Val Ser Asp Ser
305   310   315   320

Lys Gln Phe Thr Tyr Tyr Pro Leu Val Glu Asp Lys Glu Glu Val Gln
            325   330   335

Arg Lys Arg Arg Lys Ala Leu Pro Thr Phe Ser Gln Pro Phe Gly Gly
            340   345   350

Gly Ser His Met Gly Gly Gly Ser Gly Gly Ala Ala Gly Gly Tyr Gly
            355   360   365

Gly Ala Gly Gly Gly Gly Ser Leu Gly Phe Phe Pro Ser Ser Leu Ala
    370   375   380

Tyr Ser Pro Tyr Gln Ser Gly Ala Gly Pro Met Arg Cys Tyr Pro Gly
385   390   395   400

```
Gly Gly Gly Gly Ala Gln Met Ala Ala Thr Val Pro Ser Arg Asp Ser
            405                 410             415

Gly Glu Glu Ala Ala Glu Pro Ser Ala Pro Ser Arg Thr Pro Gln Cys
            420                 425             430

Glu Pro Gln Ala Pro Glu Met Leu Gln Arg Ala Arg Glu Tyr Asn Ala
            435                 440             445

Arg Leu Phe Gly Leu Ala His Ala Ala Pro Ser Pro Thr Arg Leu Leu
        450                 455             460

Arg His Arg Gly Arg Arg Ala Leu Leu Ala Gly Gln Arg His Leu Leu
465                 470             475             480

Thr Ala Gln Asp Glu Asn Gly Asp Thr Pro Leu His Leu Ala Ile Ile
            485                 490             495

His Gly Gln Thr Ser Val Ile Glu Gln Ile Val Tyr Val Ile His His
            500                 505             510

Ala Gln Asp Leu Gly Val Val Asn Leu Thr Asn His Leu His Gln Thr
            515                 520             525

Pro Leu His Leu Ala Val Ile Thr Gly Gln Thr Ser Val Val Ser Phe
        530                 535             540

Leu Leu Arg Val Gly Ala Asp Pro Ala Leu Leu Asp Arg His Gly Asp
545                 550             555             560

Ser Ala Met His Leu Ala Leu Arg Ala Gly Ala Gly Ala Pro Glu Leu
            565                 570             575

Leu Arg Ala Leu Leu Gln Ser Gly Ala Pro Ala Val Pro Gln Leu Leu
            580                 585             590

His Met Pro Asp Phe Glu Gly Leu Tyr Pro Val His Leu Ala Val Arg
        595                 600             605

Ala Arg Ser Pro Glu Cys Leu Asp Leu Leu Val Asp Ser Gly Ala Glu
        610                 615             620
```

Val Glu Ala Thr Glu Arg Gln Gly Gly Arg Thr Ala Leu His Leu Ala
625   630   635   640

Thr Glu Met Glu Glu Leu Gly Leu Val Thr His Leu Val Thr Lys Leu
                    645   650   655

Arg Ala Asn Val Asn Ala Arg Thr Phe Ala Gly Asn Thr Pro Leu His
                    660   665   670

Leu Ala Ala Gly Leu Gly Tyr Pro Thr Leu Thr Arg Leu Leu Leu Lys
                    675   680   685

Ala Gly Ala Asp Ile His Ala Glu Asn Glu Glu Pro Leu Cys Pro Leu
                    690   695   700

Pro Ser Pro Pro Thr Ser Asp Ser Asp Ser Asp Ser Glu Gly Pro Glu
705   710   715   720

Lys Asp Thr Arg Ser Ser Phe Arg Gly His Thr Pro Leu Asp Leu Thr
                    725   730   735

Cys Ser Thr Leu Val Lys Thr Leu Leu Leu Asn Ala Ala Gln Asn Thr
                    740   745   750

Met Glu Pro Pro Leu Thr Pro Pro Ser Pro Ala Gly Pro Gly Leu Ser
                    755   760   765

Leu Gly Asp Thr Ala Leu Gln Asn Leu Glu Gln Leu Leu Asp Gly Pro
                    770   775   780

Glu Ala Gln Gly Ser Trp Ala Glu Leu Ala Glu Arg Leu Gly Leu Arg
785   790   795   800

Ser Leu Val Asp Thr Tyr Arg Gln Thr Thr Ser Pro Ser Gly Ser Leu
                    805   810   815

Leu Arg Ser Tyr Glu Leu Ala Gly Gly Asp Leu Ala Gly Leu Leu Glu
                    820   825   830

Ala Leu Ser Asp Met Gly Leu Glu Glu Gly Val Arg Leu Leu Arg Gly
                    835   840   845

Pro Glu Thr Arg Asp Lys Leu Pro Ser Thr Glu Val Lys Glu Asp Ser

Ala Tyr Gly Ser Gln Ser Val Glu Gln Glu Ala Glu Lys Leu Gly Pro
865   870   875   880

Pro Pro Glu Pro Pro Gly Gly Leu Ser His Gly His Pro Gln Pro Gln
                       885   890   895

Val Thr Asp Leu Leu Pro Ala Pro Ser Pro Leu Pro Gly Pro Pro Val
                  900   905   910

Gln Arg Pro His Leu Phe Gln Ile Leu Phe Asn Thr Pro His Pro Pro
             915   920   925

Leu Ser Trp Asp Lys
        930

<210> 4
<211> 3001
<212> DNA
<213> Homo sapiens

<400> 4
actttcctgc cccttccccg gccaagccca actccggatc tcgctctcca ccggatctca   60

cccgccacac ccggacaggc ggctggagga ggcgggcgtc taaaattctg ggaagcagaa   120

cctggccgga gccactagac agagccgggc ctagcccaga gacatggaga gttgctacaa   180

cccaggtctg gatggtatta ttgaatatga tgatttcaaa ttgaactcct ccattgtgga   240

acccaaggag ccagccccag aaacagctga tggcccctac ctggtgatcg tggaacagcc   300

taagcagaga ggcttccgat ttcgatatgg ctgtgaaggc ccctcccatg gaggactgcc   360

cggtgcctcc agtgagaagg gccgaaagac ctatcccact gtcaagatct gtaactacga   420

gggaccagcc aagatcgagg tggacctggt aacacacagt gacccacctc gtgctcatgc   480

ccacagtctg gtgggcaagc aatgctcgga gctggggatc tgcgccgttt ctgtggggcc   540

caaggacatg actgcccaat taacaacct gggtgtcctg catgtgacta agaagaacat   600

gatggggact atgatacaaa aacttcagag gcagcggctc cgctctaggc cccagggcct   660

tacggaggcc gagcagcggg agctggagca gaggccaaa gaactgaaga aggtgatgga   720

tctgagtata gtgcggctgc gcttctctgc cttccttaga gccagtgatg gctccttctc   780

cctgcccctg aagccagtca cctcccagcc catccatgat agcaaatctc ggggggcatc   840

```
aaacctgaag atttctcgaa tggacaagac agcaggctct gtgcggggtg gagatgaagt       900

ttatctgctt tgtgacaagg tgcagaaaga tgacattgag gttcggttct atgaggatga       960

tgagaatgga tggcaggcct ttggggactt ctctcccaca gatgtgcata aacagtatgc      1020

cattgtgttc cggacacccc cctatcacaa gatgaagatt gagcggcctg taacagtgtt      1080

tctgcaactg aaacgcaagc gaggagggga cgtgtctgat tccaaacagt tcacctatta      1140

ccctctggtg gaagacaagg aagaggtgca gcggaagcgg aggaaggcct tgcccacctt      1200

ctcccagccc ttcgggggtg gctcccacat gggtggaggc tctgggggtg cagccggggg      1260

ctacggagga gctggaggag gtggcagcct cggtttcttc ccctcctccc tggcctacag      1320

cccctaccag tccggcgcgg gccccatgcg gtgctacccg ggaggcgggg gcgggggcgca      1380

gatggccgcc acggtgccca gcagggactc cggggaggaa gccgcggagc cgagcgcccc      1440

ctccaggacc ccccagtgcg agccgcaggc cccggagatg ctgcagcgag ctcgagagta      1500

caacgcgcgc ctgttcggcc tggcgcacgc agccccgagc cctactcgac tactgcgtca      1560

ccgcggacgc cgcgcgctgc tggcgggaca gcgccacctg ctgacggcgc aggacgagaa      1620

cggagacaca ccactgcacc tagccatcat ccacgggcag accagtgtca ttgagcagat      1680

agtctatgtc atccaccacg cccaggacct cggcgttgtc aacctcacca accacctgca      1740

ccagacgccc ctgcacctgg cggtgatcac ggggcagacg agtgtggtga gctttctgct      1800

gcgggtaggt gcagacccag ctctgctgga tcggcatgga gactcagcca tgcatctggc      1860

gctgcgggca ggcgctggtg ctcctgagct gctgcgtgca ctgcttcaga gtggagctcc      1920

tgctgtgccc cagctgttgc atatgcctga ctttgaggga ctgtatccag tacacctggc      1980

ggtccgagcc cgaagccctg agtgcctgga tctgctggtg gacagtgggg ctgaagtgga      2040

ggccacagag cggcagggggg gacgaacagc cttgcatcta gccacagaga tggaggagct      2100

ggggttggtc acccatctgg tcaccaagct ccgggccaac gtgaacgctc gcacctttgc      2160

gggaaacaca cccctgcacc tggcagctgg actggggtac ccgaccctca cccgcctcct      2220

tctgaaggct ggtgctgaca tccatgctga aaacgaggag cccctgtgcc cactgccttc      2280

accccctacc tctgatagcg actcggactc tgaagggcct gagaaggaca cccgaagcag      2340

cttccggggc cacacgcctc ttgacctcac ttgcagcacc ttggtgaaga ccttgctgct      2400

aaatgctgct cagaacacca tggagccacc cctgaccccg cccagcccag cagggccggg      2460

actgtcactt ggtgatacag ctctgcagaa cctggagcag ctgctagacg ggccagaagc      2520

ccagggcagc tgggcagagc tggcagagcg tctggggctg cgcagcctgg tagacacgta      2580
```

```
ccgacagaca acctcaccca gtggcagcct cctgcgcagc tacgagctgg ctggcggggga      2640

cctggcaggt ctactggagg ccctgtctga catgggccta gaggagggag tgaggctgct      2700

gaggggtcca gaaacccgag acaagctgcc cagcacagag gtgaaggaag acagtgcgta      2760

cgggagccag tcagtggagc aggaggcaga gaagctgggc ccaccccctg agccaccagg      2820

agggctctcg cacgggcacc cccagcctca ggtgactgac ctgctgcctg cccccagccc      2880

ccttcccgga cccctgtac agcgtcccca cctatttcaa atcttattta acaccccaca       2940

cccacccctc agttgggaca ataaaggat tctcatggga agggggaggac cccgaattcc      3000

t                                                                        3001


<210>   5
<211>   899
<212>   PRT
<213>   Mus musculus

<400>   5

Met Asp Asn Cys Tyr Asp Pro Gly Leu Asp Gly Ile Pro Glu Tyr Asp
1               5                   10                  15


Asp Phe Glu Phe Ser Pro Ser Ile Val Glu Pro Lys Asp Pro Ala Pro
            20                  25                  30


Glu Thr Ala Asp Gly Pro Tyr Leu Val Ile Val Glu Gln Pro Lys Gln
        35                  40                  45


Arg Gly Phe Arg Phe Arg Tyr Gly Cys Glu Gly Pro Ser His Gly Gly
    50                  55                  60


Leu Pro Gly Ala Ser Ser Glu Lys Gly Arg Lys Thr Tyr Pro Thr Val
65                  70                  75                  80


Lys Ile Cys Asn Tyr Glu Gly Pro Ala Lys Ile Glu Val Asp Leu Val
                85                  90                  95


Thr His Ser Asp Pro Pro Arg Ala His Ala His Ser Leu Val Gly Lys
                100                 105                 110


Gln Cys Ser Glu Leu Gly Val Cys Ala Val Ser Val Gly Pro Lys Asp
            115                 120                 125
```

```
Met Thr Ala Gln Phe Asn Asn Leu Gly Val Leu His Val Thr Lys Lys
    130                 135             140

Asn Met Met Glu Ile Met Ile Gln Lys Leu Gln Arg Gln Arg Leu Arg
145             150             155             160

Ser Lys Pro Gln Gly Leu Thr Glu Ala Glu Arg Arg Glu Leu Glu Gln
            165             170             175

Glu Ala Lys Glu Leu Lys Lys Val Met Asp Leu Ser Ile Val Arg Leu
            180             185             190

Arg Phe Ser Ala Phe Leu Arg Ala Ser Asp Gly Ser Phe Ser Leu Pro
    195             200             205

Leu Lys Pro Val Ile Ser Gln Pro Ile His Asp Ser Lys Ser Pro Gly
    210             215             220

Ala Ser Asn Leu Lys Ile Ser Arg Met Asp Lys Thr Ala Gly Ser Val
225             230             235             240

Arg Gly Gly Asp Glu Val Tyr Leu Leu Cys Asp Lys Val Gln Lys Asp
            245             250             255

Asp Ile Glu Val Arg Phe Tyr Glu Asp Asp Glu Asn Gly Trp Gln Ala
            260             265             270

Phe Gly Asp Phe Ser Pro Thr Asp Val His Lys Gln Tyr Ala Ile Val
    275             280             285

Phe Arg Thr Pro Pro Tyr His Lys Met Lys Ile Glu Arg Pro Val Thr
    290             295             300

Val Phe Leu Gln Leu Lys Arg Lys Arg Gly Gly Asp Val Ser Asp Ser
305             310             315             320

Lys Gln Phe Thr Tyr Tyr Pro Leu Val Glu Asp Lys Glu Glu Val Gln
            325             330             335

Arg Lys Arg Arg Lys Ala Leu Pro Thr Phe Ser Gln Pro Phe Gly Gly
            340             345             350

Gly Ser His Met Gly Gly Gly Ser Gly Gly Ser Ala Gly Gly Tyr Gly
```

355   360   365

Gly Ala Gly Gly Gly Gly Ser Leu Gly Phe Phe Ser Ser Ser Leu Ala
   370   375   380

Tyr Asn Pro Tyr Gln Ser Gly Ala Ala Pro Met Gly Cys Tyr Pro Gly
385   390   395   400

Gly Gly Gly Gly Ala Gln Met Ala Gly Ser Arg Arg Asp Thr Asp Ala
                   405   410   415

Gly Glu Gly Ala Glu Glu Pro Arg Thr Pro Pro Glu Ala Pro Gln Gly
                   420   425   430

Glu Pro Gln Ala Leu Asp Thr Leu Gln Arg Ala Arg Glu Tyr Asn Ala
                   435   440   445

Arg Leu Phe Gly Leu Ala Gln Arg Ser Ala Arg Ala Leu Leu Asp Tyr
   450   455   460

Gly Val Thr Ala Asp Ala Arg Ala Leu Leu Ala Gly Gln Arg His Leu
465   470   475   480

Leu Met Ala Gln Asp Glu Asn Gly Asp Thr Pro Leu His Leu